

**REMARKS**

**I. Status of the Claims/Amendments**

Claims 1-24, 27-35, 43, 44, 48-54 and 58-68 are pending. Claims 10, 21, 27, 49, 59, 62, 64, and 68 are currently amended.

The Examiner noted that claim 24 on page 5 of the previous amendment was listed as both “currently amended” and “cancelled”. In the application as filed, there were two claims numbered 24. The first was amended, the second was cancelled and presented as new claim 68.

SEQ ID NO: 6 has been resubmitted to correct an error in the originally filed listing. As indicated in Table 5, SEQ ID NO: 6 is 85 residues long, from 756-840 of SEQ ID NO: 1. Also, the transposed amino acid listings in SEQ ID NO: 7 and SEQ ID NO: 8 have been corrected to conform to the corresponding portions of SEQ ID NO: 1.

**II. Provisional Double Patenting Rejection**

Applicant requests clarification regarding the statement that SEQ ID NO: 1, 2, 4, 5, 7 and 8 of application 09/917,384 are 100% identical with the same sequences of the current application. The applicant has reviewed both sets of sequence listings and finds them to be different. The sequences of both applications are included as an appendix to this response. Since the claims address different sequences, it is respectfully requested that the Office withdraw the provisional double patenting rejection of claims 1-24, 27-35, 43, 44, 58-54 and 58-68.

**III. Rejection Under 35 U.S.C. § 101**

Claims 22-24 and 68 stand rejected because the Office asserts that the claimed invention is not supported by either a specific substantial asserted utility or a well established utility, and is not shown to be enabled. Applicant, however, contends that several utilities are asserted and supported by the specification. The instant invention is a novel cellulase from *Acidothermus cellulolyticus*, GuxA (p.1, line 10), which is “in

particular a thermal tolerant glycoside hydrolase useful in the degradation of cellulose” (p. 4, lines 8-9). As discussed on p. 3, lines 27-29, cellulase enzymes are capable of assisting in the commercial-scale processing of cellulose to sugar for use in biofuel production. Further support for the usefulness of GuxA may be found on: (p. 5, lines 6-9) GuxA may be “administered to a biomass containing cellulose for the reduction or degradation of the cellulose”; (p. 17, lines 26-30) “Like other members of the cellulase family, and in particular thermostable cellulases, GuxA polypeptides are useful in the conversion of biomass to biofuels and biofuel additives, and in particular, biofuels from cellulose. It is envisioned that GuxA polypeptides could be used for other purposes, for example in detergents, pulp and paper processing, food and feed processing, and in textile processes”; (p.27, lines 8-9) “Compositions of the present invention can be used in stonewashing jeans such as is well known in the art”; (p. 27, lines 15-16, regarding pharmaceutical compositions) “For example, GuxA polypeptides may be used where carbohydrate-mediated liposomal interactions are involved with target cells.”

Contrary to the Office assertion, the GH6 and GH12 family hydrolases do have well established and well known utilities, respectively, as the exoglucanases and endoglucanases reported on page 17 at lines 9-18 of the specification. A family comparison with the asserted catalytic domain utility is set forth in Example 2 beginning on page 33. These items are sufficient to assert utility and show operability according to expectations for the GH6 and GH12 family. For these reasons, Applicant’s attorney respectfully requests withdrawal of the rejection.

#### IV. Rejection Under 35 U.S.C. § 112, First Paragraph

Claims 22-24 and 68 stand rejected with the Office asserting that “[s]ince the claimed invention is not supported by either a asserted utility or a well established utility for the reasons set forth [in the rejection under 35 U.S.C. §101], one skilled in the art clearly would not know how to use the claimed invention.”

As discussed above, numerous utilities for the present invention were asserted in and supported by the specification. Furthermore, the specification states that enzymatic

hydrolysis of biomass (p. 2, lines 9-10) and the use of cellulase in the stonewashing of jeans (p. 27, lines 8-9) are well known. Therefore, one of ordinary skill in the art would know how to use the cellulase claimed herein in at least those capacities. For these reasons, Applicant's attorney respectfully requests withdrawal of the rejection.

**V. Rejection Under 35 U.S.C. § 112, Second Paragraph**

Claims 10, 20, 21, 49, 59, 62, 64 and 68 were rejected as indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The claims have been amended as per Examiner's suggestions. Claim 10 is now directed to "CBD II"; claims 20 and 21 recite "amino acid sequences"; claim 21 has been amended to reflect that the amino acid sequence is encoded by the nucleic acid sequence; claim 49 depends from claim 48; the word "exposed" has been removed from claim 59; claim 62 now depends from claim 59; claim 64 now depends from claim 63; and "comprises-a" has been changed to "comprises a" in claim 68. No new matter has been added to the claims as amended.

**VI. Rejection Under 35 U.S.C. § 102**

Claims 27, 35 and 43 stand rejected under 35 U.S.C. § 102(b) as being anticipated by Sakon *et al.* Sakon teaches an amino acid sequence that is 72.1% identical with SEQ ID NO: 8; however, Sakon describes a GH5 family enzyme (PAGE 10649, first column, first full paragraph). Claim 27 has been amended to recite the functionality of at least one of family GH6 and GH12, and this distinguishes Sakon. Claims 35 and 43 depend from claim 27 and should likewise be allowable.

**VII. Rejection Under 35 U.S.C. § 102/103**

Claims 1-21, 27-35, 43, 48, 54 and 58-67 stand rejected under 35 U.S.C. § 102(b) as anticipated by or, in the alternative, under 35 U.S.C. § 103(a) as obvious over either of Tucker *et al.*, Adney *et al.*, Himmel *et al.*, Lastick *et al.* or Barker *et al.* The references each teach a thermostable cellulase from *Acidothermus cellulolyticus*. The Office invites

Applicants to provide convincing proof that the cellulases of the given references are not the same as the instant enzyme.

The distinction can be shown by molecular weight comparison. The molecular weight of GUXA is 124,597 Daltons. This compares to Endo I and II having respective molecular weights of 57,420 to 74,580 as reported in Adney et al 5,366,844 (column 7, lines 61-62); 52,500 Daltons as reported in Himmel et al. 5,432,075 (see column 7, line 27 and abstract); and 156,600 to 203,400 Daltons as reported in Tucker et al. 5,110,735 (Examples 7-8).

In addition to the foregoing, Adney et al. 5,366,884 at column 10, lines 1-2 shows a sequence:

ASSDTGLFSASPTYDGVYRQGLAVAGLIAAGQHPAAAXAIDXLL.....

This sequence cannot be found in the reported sequence for GUXA which, therefore, is not shown in US 5,366,884.

As to Lastick et al., US 5,514, 584 references the cellulases described in Tucker et al. 5,110,735 (column 2, line 66 to column 3 at line 2). In like manner, Baker reports using only "endo 1," which is the same as Endo I reported in US 5,275,944 (see page 15, 4<sup>th</sup> full paragraph, chart on page 1216 denoting "A.c. E1" and footnote 31). The '944 patent is a companion case – a CIP-- to US 5,110,735 (discussed above) and is directed towards the 57,420 to 74,580 Dalton Endo 1 that is also described in US 5,110,735

The foregoing evidence is sufficient to show that the claimed GUXA is distinct because none of the reported molecular weights is even arguably 124,597 Daltons. Applicant's attorney respectfully solicits withdrawal of the rejection.

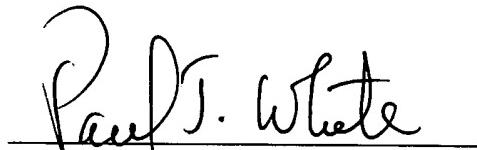
### **VIII. Conclusion**

Applicants' attorney respectfully solicits a Notice of Allowance in this application. The Commissioner is authorized to charge any additionally required fees to deposit account 14-0460. Should the Examiner have any questions, comments, or suggestions

that would expedite the prosecution of the present case to allowance, Applicants' undersigned representative earnestly requests a telephone call at (303) 384-7575.

Respectfully Submitted,

Date: 12/11/03

  
Paul J. White  
Paul J. White, Reg. No. 30,436  
Senior Patent Counsel

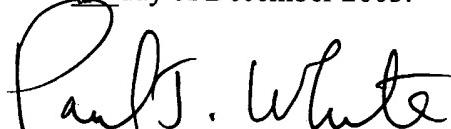
National Renewable Energy Laboratory  
1617 Cole Boulevard  
Golden, CO. 80401  
(303) 384-7575

**CERTIFICATE OF MAILING UNDER 37 CFR § 1.8**

I hereby certify that the following attached items:

1. Amendment [15 pages]
2. Statement to Support Filing and Submission in Accordance with 37 CFR 1.821-1.825
3. Replacement Figure 2
4. Marked-Up Sequence Listing [22 pages]
5. Substitute Sequence Listing [18 pages]
6. Petition and Fee for Extension of Time Under 37 CFR 1.136 and 1.17(a)(2)
7. Postcard receipt

are being deposited in the United States Postal Service as first class mail, postage prepaid, in an envelope addressed to: Commissioner for Patents, U.S. Patent & Trademark Office, P.O. Box 1450, Alexandria, Va 22313-1450 on this 11 day of December 2003.

  
Paul J. White  
Paul J. White  
Senior Patent Counsel

MARKED-UP SEQUENCE LISTING



<110> DING, SHI-YOU  
ADNEY, WILLIAM S.  
VINZANT, TODD B.  
DECKER, STEPHEN R.  
HIMMEL, MICHAEL E.

<120> THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS  
CELLULLOLYTICUS

<130> 40197.6WOOI40170.6US01

<140> 09/917,7383  
<141> 2001-07-28

<160> 14

<170> PatentIn Version: 32.1

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<211> 1228  
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<213> Artificial Sequence

<220>

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1 5 10 15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu  
20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln  
35 40 45

His Pro Ala Ile Ala Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala  
50 55 60

Thr Phe Phe Val Asn Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala  
65 70 75 80

Ala Asn Gln Thr Asn Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser  
85 90 95

Thr Tyr Ser Thr Ala Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly  
100 105 110

Val Asn Gly Gly Pro Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser  
115 120 125

Gln Gln Gln Gly Thr Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp  
130 135 140

Leu Pro Gly Arg Asp Cys Ala Ala Ser Asn Gly Glu Leu Pro  
145 150 155 160

Ala Thr Ala Ala Gly Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro  
165 170 175

Ile Ala Ser Ile Leu Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val  
180 185 190

Thr Ile Ile Glu Pro Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser  
195 200 205

Ile Gln Ala Cys Ala Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu  
210 215 220

Tyr Ala Leu Thr Lys Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met  
225 230 235 240

Asp Ala Ala His Ser Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly  
245 250 255

Tyr Val Gln Glu Val Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn  
260 265 270

Gly Ile Asp Gly Phe Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys  
275 280 285

Glu Pro Phe Met Thr Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu  
290 295 300

Ser Ala Asn Phe Tyr Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr  
305 310 315 320

Ala Val Asp Leu Tyr Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser  
325 330 335

Ile Gly Met Leu Ile Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn  
340 345 350

Glu Pro Thr Gly Pro Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn  
355 360 365

Gln Ser Lys Ile Asp Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln  
370 375 380

Asn Gly Ala Gly Leu Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe  
385 390 395 400

Pro Asn Ala His Leu Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu  
405 410 415

Ser Asp Gly Thr Ser Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser  
420 425 430

Asp Pro Met Cys Asp Pro Thr Tyr Thr Ser Tyr Gly Val Leu Thr  
435 440 445

Asn Ala Leu Pro Asn Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln  
450 455 460

Phe Asp Gln Leu Val Ala Asn Ala Arg Pro Ala Val Pro Thr Ser Thr  
465 470 475 480

Ser Ser Ser Pro Pro Pro Pro Pro Ser Pro Ser Ala Ser Pro Ser  
485 490 495

Pro Ser Pro Ser Pro Ser Pro Ser Ser Pro Ser Pro Ser Pro Ser  
500 505 510

Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser  
515 520 525

Ser Ser Pro Ser Pro Ser Pro Ser Ser Pro Ser Pro Ser Pro Ser  
530 535 540

Pro Ser Pro Ser Pro Ser Ser Pro Ser Pro Ser Pro Ser Ser Ser  
545 550 555 560

Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser  
565 570 575

Pro Ser Pro Thr Ser Ser Pro Val Ser Gly Gly Leu Lys Val Gln Tyr  
580 585 590

Lys Asn Asn Asp Ser Ala Pro Gly Asp Asn Gln Ile Lys Pro Gly Leu  
595 600 605

Gln Leu Val Asn Thr Gly Ser Ser Ser Val Asp Leu Ser Thr Val Thr  
610 615 620

Val Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser Ser Thr Leu Val Tyr  
625 630 635 640

Asn Cys Asp Trp Ala Ala Met Gly Cys Gly Asn Ile Arg Ala Ser Phe  
645 650 655

Gly Ser Val Asn Pro Ala Thr Pro Thr Ala Asp Thr Tyr Leu Gln Leu  
660 665 670

Ser Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly Ser Thr Gly Glu Ile  
675 680 685

Gln Asn Arg Val Asn Lys Ser Asp Trp Ser Asn Phe Thr Glu Thr Asn  
690 695 700

Asp Tyr Ser Tyr Gly Thr Asn Thr Thr Phe Gln Asp Trp Thr Lys Val  
705 710 715 720

Thr Val Tyr Val Asn Gly Val Leu Val Trp Gly Thr Glu Pro Ser Gly  
725 730 735

Thr Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser  
740 745 750

Pro Gly Gly Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val  
755 760 765

Thr Gly Val Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr  
770 775 780

Asp Asn Val Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu  
785 790 795 800

Val Gly Gln Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala  
805 810 815

Gly Thr Ala Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn  
820 825 830

Thr Ser Ala Pro Ser Thr Pro Val Thr Ala Thr Thr Thr Ser Pro Ser  
835 840 845

Pro Ser Pro Thr Pro Thr Gly Thr Thr Val Thr Asp Cys Thr Pro Gly  
850 855 860

Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp Glu Tyr Arg Val  
865 870 875 880

Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys Leu Thr Ile Asn  
885 890 895

Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn Phe Ser Gly Gly  
900 905 910

Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr Lys Gly Cys His  
915 920 925

Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro Ile Gln Ile Ser  
930 935 940

Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr Gln Val Ser Ser  
945 950 955 960

Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn Ser Thr Pro Thr  
965 970 975

Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile Trp Leu Asn Ser  
980 985 990

Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala Thr Gly Val Thr  
995 1000 1005

Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln Gln Thr Ser Trp  
1010 1015 1020

Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr Ser Ile Ser Asn  
1025 1030 1035 1040

Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala Arg Gly Ser Leu  
1045 1050 1055

Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly Phe Glu Ile Trp  
1060 1065 1070

Gln Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser Val Ser Val Thr  
1075 1080 1085

Ser Gly Thr Ser Ser Pro Thr Pro Ser Pro Ser Pro Thr Pro Thr Pro  
1090 1095 1100

Ser Pro Thr Pro Thr Pro Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro  
1105 1110 1115 1120

Thr Ser Ser Pro Ser Ser Gly Val Ala Cys Arg Ala Thr Tyr Val  
1125 1130 1135

Val Asn Ser Asp Trp Gly Ser Gly Phe Thr Ala Thr Val Thr Val Thr  
1140 1145 1150

Asn Thr Gly Ser Arg Ala Thr Asn Gly Trp Thr Val Ala Trp Ser Phe  
1155 1160 1165

Gly Gly Asn Gln Thr Val Thr Asn Tyr Trp Asn Thr Ala Leu Thr Gln  
1170 1175 1180

Ser Gly Ala Ser Val Thr Ala Thr Asn Leu Ser Tyr Asn Asn Val Ile  
1185 1190 1195 1200

Gln Pro Gly Gln Ser Thr Thr Phe Gly Phe Asn Gly Ser Tyr Ser Gly  
1205 1210 1215

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1220 1225

<210> 2

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<212> DNA

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tccatcggtc	cgctggcgat	gcagcatcct	gccatcgccg	cgacgcacgt	180
tatgcgggag	cgacacctt	cgtcaaccgg	tactgggccc	aagaagtaca	240
gcgaaccaga	ccaatgccac	tctcgacgc	aaaatgcgcg	tggtttcac	300
gccgtctgga	tggaccgcat	cgctgcgatc	aacggcgta	acggcgacc	360
acatatctgg	acgccccct	ctcccagcag	cagggAACCA	ccccctgaagt	420
gtcatctacg	atctgcccgg	acgcgactgc	cgccgcgtcg	cctccaaacgg	480
gctacggcag	caggTTGCA	gacctatgaa	acgcagtaca	cgatccgt	540
ctgagcaatc	cgaagfactc	cagcctcggt	atcgatgcga	tcattgagcc	600
ccaaacgcgg	tcaccaaatat	gagcattcaa	gcgtgtgcaa	cgccgggtgcc	660
caaggcatcg	agtacgcgt	cacgaaatg	cacgcattc	cgaacgtgt	720
gacGCCGCC	actccggctg	gcttgggtgg	cccaataatg	ccagcggata	780
gtccagaagg	tcccaacgc	gagcatcggt	gtcaacggca	cgtagcaggaa	840

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Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu  
20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln  
35 40 45

His Pro Ala Ile Ala  
50

<210> 4

<211> 423

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
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1 5 10 15

Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn  
20 25 30

Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala  
35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro  
50 55 60

Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gln Gly Thr  
65 70 75 80

Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp  
85 90 95

Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly  
100 105 110

Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu  
115 120 125

Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro  
130 135 140

Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala  
145 150 155 160

Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys  
165 170 175

Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser  
180 185 190

Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val  
195 200 205

Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe  
210 215 220

Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr  
225 230 235 240

Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr  
245 250 255

Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr  
260 265 270

Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile  
275 280 285

Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro  
290 295 300

Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp  
305 310 315 320

Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu  
325 330 335

Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu  
340 345 350

Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser  
355 360 365

Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp  
370 375 380

Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn  
385 390 395 400

Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val  
405 410 415

Ala Asn Ala Arg Pro Ala Val  
420

<210> 5

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
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<400> 5

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1 5 10 15

Gly Asp Asn Gln Ile Lys Pro Gly Leu Gln Leu Val Asn Thr Gly Ser  
20 25 30

Ser Ser Val Asp Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg  
35 40 45

Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met  
50 55 60

Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr  
65 70 75 80

Pro Thr Ala Asp Thr Tyr Leu Gln Leu Ser Phe Thr Gly Gly Thr Leu  
85 90 95

Ala Ala Gly Gly Ser Thr Gly Glu Ile Gln Asn Arg Val Asn Lys Ser  
100 105 110

Asp Trp Ser Asn Phe Thr Glu Thr Asn Asp Tyr Ser Tyr Gly Thr Asn  
115 120 125

Thr Thr Phe Gln Asp Trp Thr Lys Val Thr Val Tyr Val Asn Gly Val  
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Leu Val Trp Gly Thr Glu  
145 150

<210> 6

<211> 851043

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
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1 5 10 15

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20 25 30

Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu Val Gly Gln  
35 40 45

Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala Gly Thr Ala  
50 55 60

Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn Thr Ser Ala  
65 70 75 80

Pro Ser Thr Pro Val  
85  
~~Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly~~  
1        5        10        15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu  
20        25        30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln  
35        40        45

His Pro Ala Ile Ala Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala  
50        55        60

Thr Phe Phe Val Asn Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala  
65        70        75        80

Ala Asn Gln Thr Asn Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser  
85        90        95

Thr Tyr Ser Thr Ala Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly  
100      105      110

Val Asn Gly Gly Pro Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser  
115      120      125

Gln Gln Gln Gly Thr Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp  
130      135      140

Leu Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro  
145      150      155      160

Ala Thr Ala Ala Gly Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro  
165      170      175

Ile Ala Ser Ile Leu Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val  
180      185      190

Thr Ile Ile Glu Pro Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser  
195      200      205

Ile Gln Ala Cys Ala Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu  
210      215      220

Tyr Ala Leu Thr Lys Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met  
225      230      235      240

Asp Ala Ala His Ser Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly  
245      250      255

Tyr Val Gln Glu Val Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn  
260      265      270

Gly Ile Asp Gly Phe Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys  
275      280      285

Glu Pro Phe Met Thr Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu

— 290 — 295 — 300 —  
Ser Ala Asn Phe Tyr Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr  
305 310 315 320

Ala Val Asp Leu Tyr Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser  
325 330 335

Ile Gly Met Leu Ile Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn  
340 345 350

Glu Pro Thr Gly Pro Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn  
365 360 365

Gln Ser Lys Ile Asp Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln  
370 375 380

Asn Gly Ala Gly Leu Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe  
385 390 395 400

Pro Asn Ala His Leu Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu  
405 410 415

Ser Asp Gly Thr Ser Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser  
420 425 430

Asp Pro Met Cys Asp Pro Thr Tyr Thr Ser Tyr Gly Val Leu Thr  
435 440 445

Asn Ala Leu Pro Asn Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln  
450 455 460

Phe Asp Gln Leu Val Ala Asn Ala Arg Pro Ala Val Val Ser Gly Gly  
465 470 475 480

Leu Lys Val Gln Tyr Lys Asn Asn Asp Ser Ala Pro Gly Asp Asn Gln  
485 490 495

Ile Lys Pro Gly Leu Gln Leu Val Asn Thr Gly Ser Ser Ser Val Asp  
500 505 510

Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser  
515 520 525

Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met Gly Cys Gly Asn  
530 535 540

Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr Pro Thr Ala Asp  
545 550 555 560

Thr Tyr Leu Gln Leu Ser Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly  
565 570 575

Ser Thr Gly Glu Ile Gln Asn Arg Val Asn Lys Ser Asp Trp Ser Asn  
580 585 590

Phe Thr Glu Thr Asn Asp Tyr Ser Tyr Gly Thr Asn Thr Thr Phe Gln

595                  600                  605  
~~Asp Trp Thr Lys Val Thr Val Tyr Val Asn Gly Val Leu Val Trp Gly~~  
610                  615                  620  
  
~~Thr Glu Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val Thr~~  
625                  630                  635                  640  
  
~~Gly Val Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr Asp~~  
645                  650                  655  
  
~~Asn Val Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu Val~~  
660                  665                  670  
  
~~Gly Gln Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala Gly~~  
675                  680                  685  
  
~~Thr Ala Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn Thr~~  
690                  695                  700  
  
~~Ser Ala Pro Ser Thr Pro Val Asp Cys Thr Pro Gly Pro Asn Gln Asn~~  
705                  710                  715                  720  
  
~~Gly Val Thr Ser Val Gln Asp Gly Glu Tyr Arg Val Gln Thr Asn Glu~~  
725                  730                  735  
  
~~Trp Asn Ser Ser Ala Gln Gln Cys Leu Thr Ile Asn Thr Ala Thr Gly~~  
740                  745                  750  
  
~~Ala Trp Thr Val Ser Thr Ala Asn Phe Ser Gly Gly Thr Gly Gly Ala~~  
755                  760                  765  
  
~~Pro Ala Thr Tyr Pro Ser Ile Tyr Lys Gly Cys His Trp Gly Asn Cys~~  
770                  775                  780  
  
~~Thr Thr Lys Asn Val Gly Met Pro Ile Gln Ile Ser Gln Ile Gly Ser~~  
785                  790                  795                  800  
  
~~Ala Val Thr Ser Trp Ser Thr Thr Gln Val Ser Ser Gly Ala Tyr Asp~~  
805                  810                  815  
  
~~Val Ala Tyr Asp Ile Trp Thr Asn Ser Thr Pro Thr Thr Gly Gln~~  
820                  825                  830  
  
~~Pro Asn Gly Thr Glu Ile Met Ile Trp Leu Asn Ser Arg Gly Gly Val~~  
835                  840                  845  
  
~~Gln Pro Phe Gly Ser Gln Thr Ala Thr Gly Val Thr Val Ala Gly His~~  
850                  855                  860  
  
~~Thr Trp Asn Val Trp Gln Gln Gln Thr Ser Trp Lys Ile Ile Ser~~  
865                  870                  875                  880  
  
~~Tyr Val Leu Thr Pro Gly Ala Thr Ser Ile Ser Asn Leu Asp Leu Lys~~  
885                  890                  895  
  
~~Ala Ile Phe Ala Asp Ala Ala Arg Gly Ser Leu Asn Thr Ser Asp~~

900                    905                    910  
~~Tyr Leu Leu Asp Val Glu Ala Gly Phe Glu Ile Trp Gln Gly Gly Gln~~  
915                    920                    925  
  
~~Gly Leu Gly Ser Asn Ser Phe Ser Val Ser Val Thr Ser Gly Gly Val~~  
930                    935                    940  
  
~~Ala Gys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser Gly Phe~~  
945                    950                    955                    960  
  
~~Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr Asn Gly~~  
965                    970                    975  
  
~~Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr Asn Tyr~~  
980                    985                    990  
  
~~Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala Thr Asn~~  
995                    1000                    1005  
  
~~Leu Tyr Ser Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr Phe Gly~~  
1010                    1015                    1020  
  
~~Phe Asn Gly Ser Tyr Ser Gly Thr Asn Ala Ala Pro Thr Leu Ser Cys~~  
1025                    1030                    1035                    1040  
  
~~Thr Ala Ser~~

<210> 7

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
GuxA

<400> 7

Asp Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln GlyAsp  
1                    5                    10                    15

AspGly Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln  
20                    25                    30

Cys Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala  
35                    40                    45

Asn Phe Ser Gly Gly Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile  
50                    55                    60

Tyr Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met  
65                    70                    75                    80

Pro Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr  
85                    90                    95

Thr Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr  
100 105 110

Asn Ser Thr Pro Thr Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met  
115 120 125

Ile Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr  
130 135 140

Ala Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly  
145 150 155 160

Gln Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala  
165 170 175

Thr Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala  
180 185 190

Ala Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala  
195 200 205

Gly Phe Glu Ile Trp Gln Gly Gln Gly Leu Gly Ser Asn Ser Phe  
210 215 220

Ser Val Ser Val Thr Ser Gly  
225 230

<210> 8

<211> 101

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
GuxA

<400> 8

Gly Val Ala Cys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser  
1 5 10 15

Gly Phe Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr  
20 25 30

Asn Gly Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr  
35 40 45

Asn Tyr Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala  
50 55 60

Thr Asn Leu Ser Tyr Tyr Ser Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr  
65 70 75 80

Phe Gly Phe Asn Gly Ser Tyr Ser Gly Thr Asn Ala Ala Pro Thr Leu  
85 90 95

Ser Cys Thr Ala Ser  
100

<210> 9  
<211> 423  
<212> PRT  
<213> Acidothermus cellulolyticus

<400> 9

Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala Thr Phe Phe Val Asn  
1 5 10 15

Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn  
20 25 30

Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala  
35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro  
50 55 60

Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gly Thr  
65 70 75 80

Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp  
85 90 95

Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly  
100 105 110

Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu  
115 120 125

Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro  
130 135 140

Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala  
145 150 155 160

Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys  
165 170 175

Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser  
180 185 190

Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val  
195 200 205

Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe  
210 215 220

Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr  
225 230 235 240

Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr  
245 250 255

Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr  
260 265 270

Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile  
275                    280                    285

Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro  
290                    295                    300

Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp  
305                    310                    315                    320

Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu  
325                    330                    335

Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu  
340                    345                    350

Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser  
355                    360                    365

Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp  
370                    375                    380

Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn  
385                    390                    395                    400

Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln-Leu Val  
405                    410                    415

Ala Asn Ala Arg Pro Ala Val  
420

<210> 10

<211> 430

<212> PRT

<213> Cellulomonas fimi

<400> 10

Ala Pro Val His Val Asp Asn Pro Tyr Ala Gly Ala Val Gln Tyr Val  
1                    5                    10                    15

Asn Pro Thr Trp Ala Ala Ser Val Asn Ala Ala Gly Arg Gln Ser  
20                    25                    30

Ala Asp Pro Ala Leu Ala Ala Lys Met Arg Thr Val Ala Gly Gln Pro  
35                    40                    45

Thr Ala Val Trp Met Asp Arg Ile Ser Ala Ile Thr Gly Asn Ala Asp  
50                    55                    60

Gly Asn Gly Leu Lys Phe His Leu Asp Asn Ala Val Ala Gln Gln Lys  
65                    70                    75                    80

Ala Ala Gly Val Pro Leu Val Phe Asn Leu Val Ile Tyr Asp Leu Pro  
85                    90                    95

Gly Arg Asp Cys Phe Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr

100	105	110
Asp Ala Gly Leu Ala Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala		
115	120	125
Asp Leu Leu Asp Asn Pro Glu Tyr Glu Ser Ile Arg Ile Ala Ala Thr		
130	135	140
Ile Glu Pro Asp Ser Leu Pro Asn Leu Thr Thr Asn Ile Ser Glu Pro		
145	150	155
160		
Ala Cys Gln Gln Ala Ala Pro Tyr Tyr Arg Gln Gly Val Lys Tyr Ala		
165	170	175
Leu Asp Lys Leu His Ala Ile Pro Asn Val Tyr Asn Tyr Ile Asp Ile		
180	185	190
Gly His Ser Gly Trp Leu Gly Trp Asp Ser Asn Ala Gly Pro Ser Ala		
195	200	205
Thr Leu Phe Ala Glu Val Ala Lys Ser Thr Thr Ala Gly Phe Ala Ser		
210	215	220
Ile Asp Gly Phe Val Ser Asp Val Ala Asn Thr Thr Pro Leu Glu Glu		
225	230	235
240		
Pro Leu Leu Ser Asp Ser Ser Leu Thr Ile Asn Asn Thr Pro Ile Arg		
245	250	255
Ser Ser Lys Phe Tyr Glu Trp Asn Phe Asp Phe Asp Glu Ile Asp Tyr		
260	265	270
Thr Ala His Met His Arg Leu Leu Val Ala Ala Gly Phe Pro Ser Ser		
275	280	285
Ile Gly Met Leu Val Asp Thr Ser Arg Asn Gly Trp Gly Gly Pro Asn		
290	295	300
Arg Pro Thr Ser Ile Thr Ala Ser Thr Asp Val Asn Ala Tyr Val Asp		
305	310	315
320		
Ala Asn Arg Val Asp Arg Arg Val His Arg Gly Ala Trp Cys Asn Pro		
325	330	335
Leu Gly Ala Gly Ile Gly Arg Phe Pro Glu Ala Thr Pro Ser Gly Tyr		
340	345	350
Ala Ala Ser His Leu Asp Ala Phe Val Trp Ile Lys Pro Pro Gly Glu		
355	360	365
Ser Asp Gly Ala Ser Thr Asp Ile Pro Asn Asp Gln Gly Lys Arg Phe		
370	375	380
Asp Arg Met Cys Asp Pro Thr Phe Val Ser Pro Lys Leu Asn Asn Gln		
385	390	395
400		
Leu Thr Gly Ala Thr Pro Asn Ala Pro Leu Ala Gly Gln Trp Phe Glu		
405	410	415

Glu Gln Phe Val Thr Leu Val Lys Asn Ala Tyr Pro Val Ile  
420 425 430

<210> 11  
<211> 432  
<212> PRT  
<213> Thermobifida fusca

<400> 11  
Pro Gly Gly Pro Thr Asn Pro Pro Thr Asn Pro Gly Glu Lys Val Asp  
1 5 10 15

Asn Pro Phe Glu Gly Ala Lys Leu Tyr Val Asn Pro Val Trp Ser Ala  
20 25 30

Lys Ala Ala Ala Glu Pro Gly Gly Ser Ala Val Ala Asn Glu Ser Thr  
35 40 45

Ala Val Trp Leu Asp Arg Ile Gly Ala Ile Glu Gly Asn Asp Ser Pro  
50 55 60

Thr Thr Gly Ser Met Gly Leu Arg Asp His Leu Glu Glu Ala Val Arg  
65 70 75 80

Gln Ser Gly Gly Asp Pro Leu Thr Ile Gln Val Val Ile Tyr Asn Leu  
85 90 95

Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Gly Pro  
100 105 110

Asp Glu Leu Asp Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala Asp  
115 120 125

Ile Met Trp Asp Phe Ala Asp Tyr Glu Asn Leu Arg Ile Val Ala Ile  
130 135 140

Ile Glu Ile Asp Ser Leu Pro Asn Leu Val Thr Asn Val Gly Gly Asn  
145 150 155 160

Gly Gly Thr Glu Leu Cys Ala Tyr Met Lys Gln Asn Gly Gly Tyr Val  
165 170 175

Asn Gly Val Gly Tyr Ala Leu Arg Lys Leu Gly Glu Ile Pro Asn Val  
180 185 190

Tyr Asn Tyr Ile Asp Ala Ala His His Gly Trp Ile Gly Trp Asp Ser  
195 200 205

Asn Phe Gly Pro Ser Val Asp Ile Phe Tyr Glu Ala Ala Asn Ala Ser  
210 215 220

Gly Ser Thr Val Asp Tyr Val His Gly Phe Ile Ser Asn Thr Ala Asn  
225 230 235 240

Tyr Ser Ala Thr Val Glu Pro Tyr Leu Asp Val Asn Gly Thr Val Asn  
245 250 255

Gly Gln Leu Ile Arg Gln Ser Lys Trp Val Asp Trp Asn Gln Tyr Val  
260 265 270

Asp Glu Leu Ser Phe Val Gln Asp Leu Arg Gln Ala Leu Ile Ala Lys  
275 280 285

Gly Phe Arg Ser Asp Ile Gly Met Leu Ile Asp Thr Ser Arg Asn Gly  
290 295 300

Trp Gly Gly Pro Asn Arg Pro Thr Gly Pro Ser Ser Ser Thr Asp Leu  
305 310 315 320

Asn Thr Tyr Val Asp Glu Ser Arg Ile Asp Arg Arg Ile His Pro Gly  
325 330 335

Asn Trp Cys Asn Gln Ala Gly Ala Gly Leu Gly Glu Arg Pro Thr Val  
340 345 350

Asn Pro Ala Pro Gly Val Asp Ala Tyr Val Trp Val Lys Pro Pro Gly  
355 360 365

Glu Ser Asp Gly Ala Ser Glu Glu Ile Pro Asn Asp Glu Gly Lys Gly  
370 375 380

Phe Asp Arg Met Cys Asp Pro Thr Tyr Gln Gly Asn Ala Arg Asn Gly  
385 390 395 400

Asn Asn Pro Ser Gly Ala Leu Pro Asn Ala Pro Ile Ser Gly His Trp  
405 410 415

Phe Ser Ala Gln Phe Arg Glu Leu Leu Ala Asn Ala Tyr Pro Pro Leu  
420 425 430

<210> 12

<211> 221

<212> PRT

<213> Acidothermus cellulolyticus

<400> 12

Asn Gln Gln Ile Cys Asp Arg Tyr Gly Thr Thr Thr Ile Gln Asp Arg  
1 5 10 15

Tyr Val Val Gln Asn Asn Arg Trp Gly Thr Ser Ala Thr Gln Cys Ile  
20 25 30

Asn Val Thr Gly Asn Gly Phe Glu Ile Thr Gln Ala Asp Gly Ser Val  
35 40 45

Pro Thr Asn Gly Ala Pro Lys Ser Tyr Pro Ser Val Tyr Asp Gly Cys  
50 55 60

His Tyr Gly Asn Cys Ala Pro Arg Thr Thr Leu Pro Met Arg Ile Ser

65	70	75	80
Ser Ile Gly Ser Ala Pro Ser Ser Val Ser Tyr Arg Tyr Thr Gly Asn			
85	90	95	
Gly Val Tyr Asn Ala Ala Tyr Asp Ile Trp Leu Asp Pro Thr Pro Arg			
100	105	110	
Thr Asn Gly Val Asn Arg Thr Glu Ile Met Ile Trp Phe Asn Arg Val			
115	120	125	
Gly Pro Val Gln Pro Ile Gly Ser Pro Val Gly Thr Ala His Val Gly			
130	135	140	
Gly Arg Ser Trp Glu Val Trp Thr Gly Ser Asn Gly Ser Asn Asp Val			
145	150	155	160
Ile Ser Phe Leu Ala Pro Ser Ala Ile Ser Ser Trp Ser Phe Asp Val			
165	170	175	
Lys Asp Phe Val Asp Gln Ala Val Ser His Gly Leu Ala Thr Pro Asp			
180	185	190	
Trp Tyr Leu Thr Ser Ile Gln Ala Gly Phe Glu Pro Trp Glu Gly Gly			
195	200	205	
Thr Gly Leu Ala Val Asn Ser Phe Ser Ser Ala Val Asn			
210	215	220	
<210> 13			
<211> 221			
<212> PRT			
<213> Streptomyces sp.			
<400> 13			
Asp Thr Thr Ile Cys Glu Pro Phe Gly Thr Thr Thr Ile Gln Gly Arg			
1	5	10	15
Tyr Val Val Gln Asn Asn Arg Trp Gly Ser Thr Ala Pro Gln Cys Val			
20	25	30	
Thr Ala Thr Asp Thr Gly Phe Arg Val Thr Gln Ala Asp Gly Ser Ala			
35	40	45	
Pro Thr Asn Gly Ala Pro Lys Ser Tyr Pro Ser Val Phe Asn Gly Cys			
50	55	60	
His Tyr Thr Asn Cys Ser Pro Gly Thr Asp Leu Pro Val Arg Leu Asp			
65	70	75	80
Thr Val Ser Ala Ala Pro Ser Ser Ile Ser Tyr Gly Phe Val Asp Gly			
85	90	95	
Ala Val Tyr Asn Ala Ser Tyr Asp Ile Trp Leu Asp Pro Thr Ala Arg			
100	105	110	
Thr Asp Gly Val Asn Gln Thr Glu Ile Met Ile Trp Phe Asn Arg Val			

115                    120                    125

Gly Pro Ile Gln Pro Ile Gly Ser Pro Val Gly Thr Ala Ser Val Gly  
130                    135                    140

Gly Arg Thr Trp Glu Val Trp Ser Gly Gly Asn Gly Ser Asn Asp Val  
145                    150                    155                    160

Leu Ser Phe Val Ala Pro Ser Ala Ile Ser Gly Trp Ser Phe Asp Val  
165                    170                    175

Met Asp Phe Val Arg Ala Thr Val Ala Arg Gly Leu Ala Glu Asn Asp  
180                    185                    190

Trp Tyr Leu Thr Ser Val Gln Ala Gly Phe Glu Pro Trp Gln Asn Gly  
195                    200                    205

Ala Gly Leu Ala Val Asn Ser Phe Ser Ser Thr Val Glu  
210                    215                    220

<210> 14

<211> 228

<212> PRT

<213> Streptomyces lividans

<400> 14

Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp  
1                    5                    10                    15

Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys  
20                    25                    30

Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn  
35                    40                    45

Phe Ser Gly Gly Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr  
50                    55                    60

Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro  
65                    70                    75                    80

Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr  
85                    90                    95

Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn  
100                    105                    110

Ser Thr Pro Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile  
115                    120                    125

Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala  
130                    135                    140

Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln  
145                    150                    155                    160

Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr

165                  170                  175

Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala  
180                  185                  190

Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly  
195                  200                  205

Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser  
210                  215                  220

Val Ser Val Thr  
225